AMENDMENTS TO THE SPECIFICATION

Please amend the specification as follows. Insertions are shown <u>underlined</u> while deletions are struck through.

The paragraph beginning at page 34, line 10:

The Pv$_{GR}$ cDNA (NCBI access number: AF139644) is a ~~1764~~<u>1765</u> bp long fragment. The start codon was found 25 bp downstream from the cDNA 5'terminus, which follows the PstI restriction site of pBluescript polylinker. An open reading frame of 1635 bp, which codes for a 545 amino acid long polypeptide was found. After the stop codon, a 105 bp long 3' untranslated region followed by a terminal 26 bp poly-A tail was found.

The paragraph beginning at page 13, line 1:

The determination of percent identity between two sequences can be accomplished using a mathematical algorithm. A preferred, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin et al. (*Proc. Natl. Acad. Sci.* USA, 90:5873-5877 (1993)). Such an algorithm is incorporated into the NBLAST program which can be used to identify sequences having the desired identity to nucleotide sequences of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al. (*Nucleic Acids Res*, 25:3389-3402 (1997)). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., NBLAST) can be used. ~~See http://www.ncbi.nlm.nih.gov.~~ In one embodiment, parameters for sequence comparison can be set at W=12. Parameters can also be varied (e.g., W=5 or W=20). The value "W" determines how many continuous nucleotides must be identical for the program to identify two sequences as containing regions of identity.